SCORE Search Results Details for Application 10747994 and Search Result us-10-747-994-2.rag.

This page gives you Search Results detail for the Application 10747994 and Search Result us-10-747-994-2.rag.

start

```
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OM protein - protein search, using sw model

Run on:          May 30, 2006, 14:37:59 ; Search time 87 Seconds
                                          (without alignments)
                                          1813.100 Million cell updates/sec

Title:           US-10-747-994-2
Perfect score:   1804
Sequence:        1 MSFYPCNTTASVRSGNSATV.........PLLYRNWHCHFYQTNVESSL 345

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:     2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_8:*
                 1:   geneseqp1980s:*
                 2:   geneseqp1990s:*
                 3:   geneseqp2000s:*
                 4:   geneseqp2001s:*
                 5:   geneseqp2002s:*
                 6:   geneseqp2003as:*
                 7:   geneseqp2003bs:*
                 8:   geneseqp2004s:*
                 9:   geneseqp2005s:*
                 10:  geneseqp2006s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                          SUMMARIES
```

SCORE Search Results Details for Application 10747994 and Search Result us-10-747-994-2.ra

This page gives you Search Results detail for the Application 10747994 and Search Result us-10-74 994-2.rai.

```
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OM protein - protein search, using sw model

Run on:          May 30, 2006, 14:44:59 ; Search time 49 Seconds
                                           (without alignments)
                                           616.287 Million cell updates/sec

Title:           US-10-747-994-2
Perfect score:   1804
Sequence:        1 MSFYPCNTTASVRSGNSATV..........PLLYRNWHCHFYQTNVESSL 345

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters:        650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_AA:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
                 2:  /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
                 3:  /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                 7:  /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.


                              SUMMARIES
                     %
Result            Query
   No.    Score  Match Length DB  ID                      Description
-----------------------------------------------------------------------------
     1    1342   74.4    359  1   US-08-812-203-3         Sequence 3, Appli
```

SCORE Search Results Details for Application 10747994 and Search Result us-10-747-994-2.ra

This page gives you Search Results detail for the Application 10747994 and Search Result us-10-7‹ 2.rapbm.

start

Go Back to pr‹

```
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OM protein - protein search, using sw model

Run on:         May 30, 2006, 14:45:44 ; Search time 183 Seconds
                                         (without alignments)
                                         873.274 Million cell updates/sec

Title:          US-10-747-994-2
Perfect score:  1804
Sequence:       1 MSFYPCNTTASVRSGNSATV..........PLLYRNWHCHFYQTNVESSL 345

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:     2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_AA_Main:*
                1:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1804	100.0	345	5	US-10-747-994-2	Sequence 2, Appli
2	1342	74.4	359	4	US-10-225-567A-287	Sequence 287, App
3	1342	74.4	359	5	US-10-689-861-4	Sequence 4, Appli

SCORE Search Results Details for Application 10747994 and Search Result us-10-747-994-2.ra

This page gives you Search Results detail for the Application 10747994 and Search Result us-10-7ₐ
2.rapbn.

start

Go Back to pr₁

```
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OM protein - protein search, using sw model

Run on:         May 30, 2006, 14:46:39 ; Search time 16 Seconds
                                         (without alignments)
                                         240.149 Million cell updates/sec

Title:          US-10-747-994-2
Perfect score:  1804
Sequence:       1 MSFYPCNTTASVRSGNSATV..........PLLYRNWHCHFYQTNVESSL 345

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters:      56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_AA_New:*
           1:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
           2:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
           3:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
           4:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
           5:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
           6:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
           7:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
           8:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.


                              SUMMARIES
                    %
Result            Query
   No.   Score   Match  Length  DB   ID                        Description
-------------------------------------------------------------------------------
     1   540.5    30.0     289   7   US-11-293-697-3907         Sequence 3907, Ap
```

SCORE Search Results Details for Application 10: 747-994-2.rpr.

This page gives you Search Results detail for the Application 10747994 and Search Result us-10-7‹

start

```
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OM protein - protein search, using sw model

Run on:         May 30, 2006, 14:39:54 ; Search time 40 Seconds
                                          (without alignments)
                                          829.870 Million cell updates/sec

Title:          US-10-747-994-2
Perfect score:  1804
Sequence:       1 MSFYPCNTTASVRSGNSATV.........PLLYRNWHCHFYQTNVESSL 345

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:        283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      PIR_80:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1342	74.4	359	2	I39153	prostanoid DP rece
2	911.5	50.5	231	2	I59269	prostaglandin D re
3	711	39.4	362	2	S66674	prostaglandin E re
4	700.5	38.8	358	2	I38920	prostaglandin E2 r
5	697.5	38.7	358	2	S51312	EP2 prostaglandin
6	626.5	34.7	417	2	A54416	prostacyclin recep